



## SEQUENCE LISTING

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<120> USE OF METALLIC CATIONS TO IMPROVE FUNCTIONAL ACTIVITY OF  
ANTIBODIES

<130> 096183-0104

<140> 10/576,440

<141> 2007-03-23

<150> PCT/FR2004/002687

<151> 2004-10-20

<150> FR 0312228

<151> 2003-10-20

<160> 2

<170> PatentIn version 3.5

<210> 1

<211> 1428

<212> DNA

<213> Homo sapiens

<220>

<223> cDNA sequence of double mutant His310-435Lys

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gccaaagggg tggagtgggt ggcaactata tcatatgatg gaaggaatat acaatatgca	240
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gtcaccgtct cttcagcctc caccaagggc ccatcggtct tccccctggc accctcctcc	480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	540
ccggtgacgg tgctcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccggt	600
gtcctacagt cctcaggact ctactcctc agcagcgtgg tgaccgtgcc ctccagcagc	660

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gaactcctgg ggggaccgtc agtcttcttc ttcccccaa aaccaagga caccctcatg      840
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tggtgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc     1080
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc     1140
ccatccccggg atgagctgac caagaaccag gtcagcctga cctgcctggg caaaggcttc     1200
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag     1260
accacgcctc ccggtgctgga ctccgacggc tccttcttcc tctacagcaa gctcacctg      1320
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgatgatgca tgaggctctg      1380
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<210> 2

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<212> PRT

<213> Homo sapiens

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<223> Peptide sequence of double mutant His310-H435Lys.

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Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20           25           30

```

```

Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35           40          45

```

```

Lys Asn Tyr Ala Met His Trp Val Arg Gln Ala Pro Ala Lys Gly Leu
50           55          60

```

```

Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Arg Asn Ile Gln Tyr Ala
65           70          75          80

```

```

Asp Ser Val Lys Gly Arg Cys Thr Phe Ser Arg Asp Asn Ser Gln Asp
85           90          95

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Thr Leu Tyr Leu Gln Leu Asn Ser Leu Arg Pro Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Pro Val Arg Ser Arg Trp Leu Gln Leu Gly Leu  
 115 120 125

Glu Asp Ala Phe His Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser  
 130 135 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
 145 150 155 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
 165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
 180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
 195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
 210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
 225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro  
 245 250 255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
 260 265 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
 275 280 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
 290 295 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
 305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
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Leu Lys Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
                   340                                  345                                  350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
                   355                                  360                                  365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
                   370                                  375                                  380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
                   385                                  390                                  395                                  400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
                   405                                  410                                  415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
                   420                                  425                                  430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
                   435                                  440                                  445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Lys Tyr  
                   450                                  455                                  460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                   465                                  470                                  475